

1/5

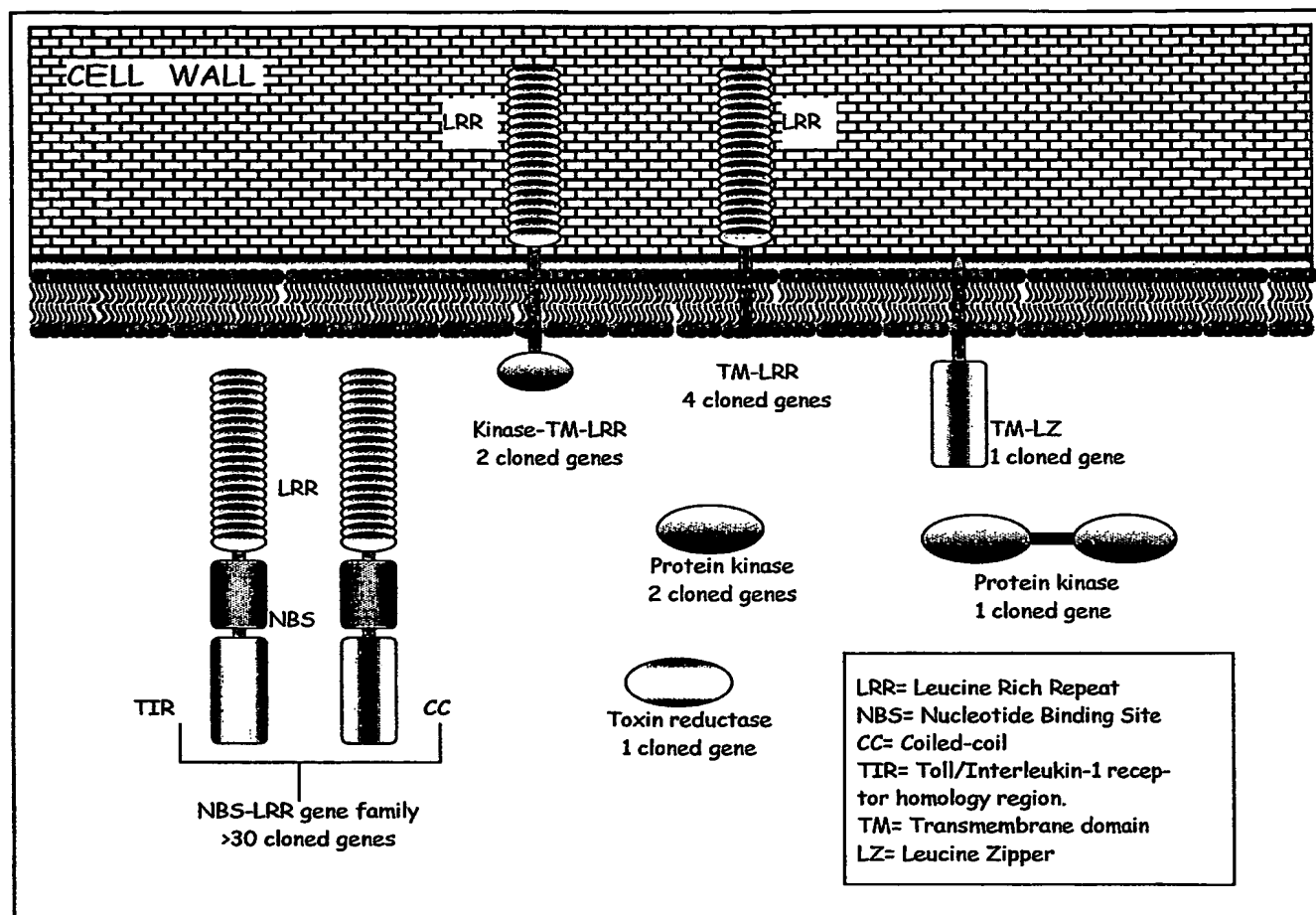


FIGURE 1

2/5

		10	20	30	40	50	60	
RGA5	1	MS	TALVIGGWFAQSFIQTLLDKASNCATQOLARRRGLHDDLRRTSLLRIHAILDKAET	60				
RGA2	1	-MADVTPOAAAVFSLVNEIFNRSINLIVAEIRLOLNARAEINNORTLLRTHSLLEEAKA	59					
		70	80	90	100	110	120	
RGA5	61	RWNHKN	TSLV	ELVR	OLKDAAYDAEELLLEEL	EYQAAK	OKVEHRGDQISDLFSFSLSTASEW	120
RGA2	60	RR-MT	DKSLV	LWLMELKEWAYDADDILDEYFAAAIRLKVTR	---	S----	TFKRLIDHVI	110
		130	140	150	160	170	180	
RGA5	121	LGADGDDAGT	RLREI	OGKLCNIAADMM	DVMQLAPDDGGRO	FDWKVVRRETSSFLTETVV	180	
RGA2	111	INVP---	LAHKVADIRKRL	NGVTLERELNLGALE---	GSQPLDS	-TKRGVITSLLTESCI	163	
		190	200	210	220	230	240	
RGA5	181	FGNDQEREK	VVELLL	DSGSGNSSFSVL	PLVGI	GGVGKTTLAQLVYNDNRVGN	YFHLKVWV	240
RGA2	164	VGRAQDKENLIRLL	LEPSDG--	AVFV	VEIVGLGCAGKTTLSQLIFNDKRV	EEHFPLRMWV	221	
		250	260	270	280	290	300	
RGA5	241	CVSDN	FNVKRLTKEI	IESATKVEQSDKLNLD	TLQOILKFKIASERFLLVI	DDVWSFNRRDD	300	
RGA2	222	CVSDDE	DVKRITREITEY	ATNGRFMLTNLNLQVNLKEEIRGT	TFLVLDDVWNE	DPVK	281	
		310	320	330	340	350	360	
RGA5	301	WERICAPL	RFARGSKVIV	TTRDTKIASITIGTMKEISLDGL	ODDAYWELEKKCAF	GSVN-	359	
RGA2	282	WESLLAPLDAGGR	GSVVIVTTQSKKVADVTGTMEPYVLEEIT	EDDSWSLIESHSFREASC	341			
		370	380	390	400	410	420	
RGA5	360	PQEHLE	LEVIGRKIAGNLKGSPLAAKT	LGSLRLLDVSOEHWR	TIMSEVWOLPOAENEIL	419		
RGA2	342	SSTNPRMEEIGRKIAK	KISGLPYGATAMGRYLRSKHGESSWREVLE	TETWEMPPAASDVL	401			
		430	440	450	460	470	480	
RGA5	420	PVLWLSYQHL	PGHIDROCFAFC	AVFHKDYLFYKHETIQTWIAEGFTIAHQGN	KRMEDVGSSY	479		
RGA2	402	SALRRSYDNL	PPOLKLCFAFCALFTKGYRFRKDTLIH	MWIAONLIQSTESKRSELM	AECEC	461		
		490	500	510	520	530	540	
RGA5	480	FHEI	VNRSFFQESRWRCGR	YVMHDLIHLLAQFISVGECHR	IDDKSKETESTTRIL	SVALT	539	
RGA2	462	FDDIVCREFFERY	S--WGNVMNDSVHDLARWVSLDEYFRAED	DSPLHISKPIRHL	SWCSE	519		
		550	560	570	580	590	600	
RGA5	540	EQMKLV	DFSGYN-KLRTL	MNNQNOYPYMTKVNSCLIPHS	LKRLKRIHV	LVLOKQGMK	598	
RGA2	520	RITNVLED	NNTGDAVNPLSSLR	TLLFLGQSEFRSYHLLDRM	FRMLSRIRV	LDSENVIR	579	

FIGURE 2-1

3/5

		610	620	630	640	650	660	
RGA5	599	ELPDITIGDLIQIRYLDISYNACTQRLPESLCDLYNLCATRLWGCOLRSEFQGM SKLINLR	658					
RGA2	580	NLPSSVGNLKHIRYLGLS-NTRIQRLPESVTRLCCLQTLLECELCRLPRSMSRI VKLR	638					
		670	680	690	700	710	720	
RGA5	659	QLRVEDEITSKIYEVGKLISLQELSAFKVLNNHGNKTAELSGITQIRSTLRITNLENVGS	718					
RGA2	639	QLKANPDVIADI AKVGRLIELQELKAYNVDDKKKGHTAELSAMNQLHGDLSIRNQLONVEK	698					
		730	740	750	760	770	780	
RGA5	719	KELASKAKLHRKQYIEALELEWAAGQVSSLEHPELLVSEEVILGLQPHHFLKSLTIRGYSG	778					
RGA2	699	TRESRKARLDEKOKIKLLDLRWADGRG---AGECDRDRKVLKGLRPHPNLRELSIKYYGG	755					
		790	800	810	820	830	840	
RGA5	779	ATVPSWLDVKKMLPNLGTILKLENCTRIEGLSYIGQLPHLKVLMKRMVVKOMSHELCGCT	838					
RGA2	756	TSSPSWMTDOYLPNMETIRLRSCARLTLEPCLGQLHILRHLHIDGMSOVROINLOFYGTG	815					
		850	860	870	880	890	900	
RGA5	839	KSKLFPRLLEELVLEDMPTLKKEEPNLAQLPCLKIHMKNMFAVKHIGRELYGDIESNCFLS	898					
RGA2	816	EVSGFPILLELINIRRMFSLEEWS-----EP	840					
		910	920	930	940	950	960	
RGA5	899	LEELVLQDMLTLEELPNLGQLPHLKVLIHMKNMSALKLIGRELCDSEKIWFPRLEVLVLK	958					
RGA2	840	-----R-----RNCCYFPR-----	849					
		970	980	990	1000	1010	1020	
RGA5	959	NMLALEELPSLDNFRVSRFFASSVEVGHLFSATRKNWFPRLEELEIKGMLTFEELHSLE	1018					
RGA2	849	-----LH-----	851					
		1030	1040	1050	1060	1070	1080	
RGA5	1019	KLPCLKVFRIGKLPVKKIGHGLFDSTCQRECFPRLEDLVLSMPAWEESWAEREELFS	1078					
RGA2	851	-----	851					
		1090	1100	1110	1120	1130	1140	
RGA5	1079	CLCRIKIEQCPKIKCLLPPIPHSLIKLELWQVGLTGLPGLCKGIGGGSSTRTASLSLHII	1138					
RGA2	851	---KLLIEDCPRLRNLPISLPPTLEELRTISRTGLVDLPG-FH---ENGDTVNTVSLSLHVS	905					
		1150	1160	1170	1180	1190	1200	
RGA5	1139	KCPNLRNIGEGLLSNHPTINAIRIWECAELLWLFPVKRFREFTTLENLSTRNCPKLMSMT	1198					
RGA2	906	ECRELRSLSEGLLOHNVALKTAFTDCDSLEFLPAEGFRTAISLESIMTNCP--LPQS	963					

FIGURE 2-2

4/5

		1210	1220	1230	1240	1250	1260	
RGA5	1199	QCEENDLLLPPLIKALELGDG	---	NLGKSLPGCLHNLS	SLTQLAISNCPYMVSL	PREVM		1255
RGA2	963	-----FLIPSSLEHLKIQPCLYPNNEDSI	STCFENLTSLSFIDIKDCPNLSSEFP	PGPI				1017
		1270	1280	1290	1300	1310	1320	
RGA5	1256	LHLKELGTVRIENC	DGLGSL	EGLVKSLKRLAIGCPRL	LLNE	-----	GDEQGEVLS	1308
RGA2	1018	COLSALOHL	SLVNCORLOSIG	-EQALTSLES	LTIONCPRLTMSHSLVEVNNSSDT	G	LAFN	1076
		1330	1340	1350	1360	1370	1380	
RGA5	1309	LLELSVDKT	---	ALLKLSLTKN	-----	TLPFIHSLRIIWS	PQKVMFDLEE	QELVHS 1356
RGA2	1077	ITRWRRRT	TGDDGLMLRHRAQ	NDSSFGLLOHL	TFLOFLKICQCPQ	LVTFTEGEE	EKKWRN 1136	
		1390	1400	1410	1420	1430	1440	
RGA5	1357	ITAIRRT	EEFRCKNLS	LPTELHTLPSL	HALVSDCPQIQSL	PEKGLPTLLTDI	GFDHCH 1416	
RGA2	1137	ITSTQIIHIVD	CPNLEVL	PANLOS	LCSTSTIYLVRCPRI	HAFPPGGVSM	SLAHIVTHECP 1196	
		1450	1460	1470				
RGA5	1417	PVLT	-----	AQLEKHLAEMK	---	SSGRFHPVYA	---	1441
RGA2	1197	QICQRC	DPFGDDWPLIANV	PRICLGRTHPCRC	STT			1232

FIGURE 2-3

5/5

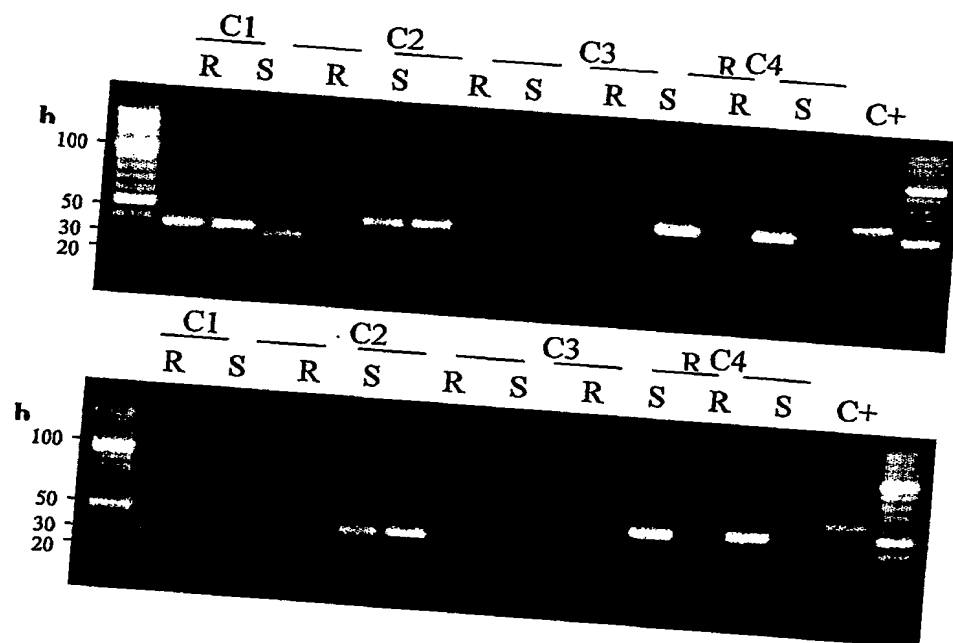


FIGURE 3